

Patent Application US/07/752,427

A circular icon with the letters 'OK' inside, indicating a successful or acceptable state.

## **SEQUENCE LISTING**

**(1) GENERAL INFORMATION:**

(i) APPLICANT: Grotendorst, Gary R.  
Bradham Jr., Douglas M.,

(ii) TITLE OF INVENTION: CONNECTIVE TISSUE GROWTH FACTOR

**(iii) NUMBER OF SEQUENCES: 2**

**(iv) CORRESPONDENCE ADDRESS:**

(A) ADDRESSEE: Spensley Horn Jubas & Lubitz  
(B) STREET: 4225 Executive Square, Suite 1400  
(C) CITY: La Jolla  
(D) STATE: CA  
(E) COUNTRY: US  
(F) ZIP: 92037

(v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: US  
(B) FILING DATE: 30-AUG-1991  
(C) CLASSIFICATION:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Wetherell, Jr: Ph.D., John W.  
(B) REGISTRATION NUMBER: 31,678  
(C) REFERENCE/DOCKET NUMBER: PD-1294

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 619-455-5100  
(B) TELEFAX: 619-455-5110

**(2) INFORMATION FOR SEQ ID NO:1:**

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 2075 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

**(vii) IMMEDIATE SOURCE:**

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54 (B) CLONE: DB60R32

55

56 (ix) FEATURE:

57 (A) NAME/KEY: CDS

58 (B) LOCATION: 130..1177

59

60

61 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

62

63 CCCGGCCGAC	AGCCCCGAGA	CGACAGCCCC	GCGCGTCCCG	GTCCCCACCT	CCGACCCACCG	60
64						
65 CCAGCGCTCC	AGGCCCCGCG	CTCCCCGCTC	GCCGCCACCG	CGCCCTCCGC	TCCGCCCGCA	120
66						
67 GTGCCAACCC	ATG ACC GCC	GCC AGT ATG	GGC CCC GTC	CGC GTC GCC	TTC	168
68	Met Thr Ala	Ala Ser Met	Gly Pro Val	Arg Val Ala	Phe	
69	1	5	10			
70						
71 GTG GTC CTC CTC	GCC CTC TGC	AGC CGG CCG	GCC GTC GGC	CAG AAC TGC	216	
72 Val Val Leu	Leu Ala Leu	Cys Ser Arg	Pro Ala Val	Gly Gln Asn	Cys	
73	15	20	25			
74						
75 AGC GGG CCG TGC	CGG TGC CCG	GAC GAG CCG	GCG CCG CGC	TGC CCG GCG	264	
76 Ser Gly Pro Cys	Arg Cys Pro Asp	Glu Pro Ala	Pro Arg Cys	Pro Ala		
77	30	35	40	45		
78						
79 GGC GTG AGC CTC	GTG CTG GAC	GGC TGC GGC	TGC CGC GTC	TGC GCC	312	
80 Gly Val Ser Leu	Val Leu Asp	Gly Cys Gly	Cys Cys Arg	Val Cys Ala		
81	50	55	60			
82						
83 AAG CAG CTG GGC	GAG CTG TGC	ACC GAG CGC	CCC TGC GAC	CCG CAC	360	
84 Lys Gln Leu	Gly Glu Leu	Cys Thr	Glu Arg Asp	Pro Cys Asp	Pro His	
85	65	70	75			
86						
87 AAG GGC CTC TTC	TGT GAC TTC	GGC TCC CCG	GCC AAC CGC	AAG ATC GGC	408	
88 Lys Gly Leu	Phe Cys Asp	Phe Gly Ser	Pro Ala Asn	Arg Lys Ile	Gly	
89	80	85	90			
90						
91 GTG TGC ACC	GCC AAA GAT	GGT GCT CCC	TGC ATC TTC	GGT GGT ACG GTG	456	
92 Val Cys Thr Ala	Lys Asp	Gly Ala Pro	Cys Ile Phe	Gly Thr Val		
93	95	100	105			
94						
95 TAC CGC AGC GGA	GAG TCC TTC	CAG AGC AGC	TGC AAG TAC	CAG TGC ACG	504	
96 Tyr Arg Ser	Gly Glu Ser	Phe Gln Ser	Ser Cys Lys	Tyr Gln Cys	Thr	
97	110	115	120	125		
98						
99 TGC CTG GAC	GGG GCG GTG	GGC TGC ATG	CCC CTG TGC AGC	ATG GAC GTT	552	
100 Cys Leu Asp	Gly Ala Val	Gly Cys Met	Pro Leu Cys	Ser Met Asp	Val	
101	130	135	140			
102						
103 CGT CTG CCC AGC	CCT GAC TGC	CCC TTC CCG	AGG AGG GTC	AAG CTG CCC	600	
104 Arg Leu Pro	Ser Pro Asp	Cys Pro Phe	Pro Arg Arg	Val Lys Leu	Pro	
105	145	150	155			
106						

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107	GGG AAA TGC TGC GAG GAG TGG GTG TGT GAC GAG CCC AAG GAC CAA ACC	648		
108	Gly Lys Cys Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr			
109	160	165	170	
110				
111	G TG GTT GGG CCT GCC CTC GCG GCT TAC CGA CTG GAA GAC ACG TTT GGC	696		
112	Val Val Gly Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly			
113	175	180	185	
114				
115	CCA GAC CCA ACT ATG ATT AGA GCC AAC TGC CTG GTC CAG ACC ACA GAG	744		
116	Pro Asp Pro Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu			
117	190	195	200	205
118				
119	TGG AGC GCC TGT TCC AAG ACC TGT GGG ATG GGC ATC TCC ACC CGG GTT	792		
120	Trp Ser Ala Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val			
121	210	215	220	
122				
123	ACC AAT GAC AAC GCC TCC TGC AGG CTA GAG AAG CAG AGC CGC CTG TGC	840		
124	Thr Asn Asp Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys			
125	225	230	235	
126				
127	ATG GTC AGG CCT TGC GAA GCT GAC CTG GAA GAG AAC ATT AAG AAG GGC	888		
128	Met Val Arg Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly			
129	240	245	250	
130				
131	AAA AAG TGC ATC CGT ACT CCC AAA ATC TCC AAG CCT ATC AAG TTT GAG	936		
132	Lys Lys Cys Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu			
133	255	260	265	
134				
135	CTT TCT GGC TGC ACC AGC ATG AAG ACA TAC CGA GCT AAA TTC TGT GGA	984		
136	Leu Ser Gly Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly			
137	270	275	280	285
138				
139	GTA TGT ACC GAC GGC CGA TGC TGC ACC CCC CAC AGA ACC ACC ACC CTG	1032		
140	Val Cys Thr Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Leu			
141	290	295	300	
142				
143	CCG GTG GAG TTC AAG TGC CCT GAC GGC GAG GTC ATG AAG AAG AAC ATG	1080		
144	Pro Val Glu Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met			
145	305	310	315	
146				
147	ATG TTC ATC AAG ACC TGT GCC TGC CAT TAC AAC TGT CCC GGA GAC AAT	1128		
148	Met Phe Ile Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn			
149	320	325	330	
150				
151	GAC ATC TTT GAA TCG CTG TAC TAC AGG AAG ATG TAC GGA GAC ATG GCA T	1177		
152	Asp Ile Phe Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala			
153	335	340	345	
154				
155	GAAGCCAGAG AGTGAGAGAC ATTAACATCAT TAGACTGGAA CTTGAACTGA TTCACTCTC	1237		
156				
157	ATTTTCCGT AAAATGATT TCAGTAGCAC AAGTTATTTA AATCTGTTTT TCTAACTGGG	1297		
158				
159	GGAAAAGATT CCCACCCAAT TCAAAACATT GTGCCATGTC AAACAAATAG TCTATCTTCC	1357		

160  
161 CCAGACACTG GTTTGAAGAA TGTAAAGACT TGACAGTGG ACTACATTAG TACACAGCAC 1417  
162  
163 CAGAATGTAT ATTAAGGTGT GGCTTTAGGA GCAGTGGGAG GGTACCGGCC CGGTTAGTAT 1477  
164  
165 CATCAGATCG ACTCTTATAC GAGTAATATG CCTGCTATTT GAAGTGTAAT TGAGAAGGAA 1537  
166  
167 AATTTAGCG TGCTCACTGA CCTGCCTGTA GCCCCAGTGA CAGCTAGGAT GTGCATTCTC 1597  
168  
169 CAGCCATCAA GAGACTGAGT CAAGTTGTT CTTAACAGTCAG AACAGCAGAC TCAGCTCTGA 1657  
170  
171 CATTCTGATT CGAATGACAC TGTTCAAGGAA TCGGAATCCT GTCGATTAGA CTGGACAGCT 1717  
172  
173 TGTGGCAAGT GAATTTGCCT GTAACAAGCC AGATTTTTA AAATTTATAT TGTAAATATT 1777  
174  
175 GTGTGTGTGT GTGTGTGTGT ATATATATAT ATATATGTAC AGTTATCTAA GTTAATTAA 1837  
176  
177 AGTTGTTGT GCCTTTTAT TTTGTTTT AATGCTTTGA TATTCAATG TTAGCCTCAA 1897  
178  
179 TTTCTGAACA CCATAGGTAG AATGTAAAGC TTGTCTGATC GTTCAAAGCA TGAAATGGAT 1957  
180  
181 ACTTATATGG AAATTCTGCT CAGATAGAAT GACAGTCCGT CAAAACAGAT TGTTGCAAA 2017  
182  
183 GGGGAGGCAT CAGTGTCTTG GCAGGCTGAT TTCTAGGTAG GAAATGTGGT AGCTCACG 2075  
184  
185  
186 (2) INFORMATION FOR SEQ ID NO:2:  
187  
188 (i) SEQUENCE CHARACTERISTICS:  
189 (A) LENGTH: 349 amino acids  
190 (B) TYPE: amino acid  
191 (D) TOPOLOGY: linear  
192  
193 (ii) MOLECULE TYPE: protein  
194  
195 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:  
196  
197 Met Thr Ala Ala Ser Met Gly Pro Val Arg Val Ala Phe Val Val Leu  
198 1 5 10 15  
199  
200 Leu Ala Leu Cys Ser Arg Pro Ala Val Gly Gln Asn Cys Ser Gly Pro  
201 20 25 30  
202  
203 Cys Arg Cys Pro Asp Glu Pro Ala Pro Arg Cys Pro Ala Gly Val Ser  
204 35 40 45  
205  
206 Leu Val Leu Asp Gly Cys Gly Cys Cys Arg Val Cys Ala Lys Gln Leu  
207 50 55 60  
208  
209 Gly Glu Leu Cys Thr Glu Arg Asp Pro Cys Asp Pro His Lys Gly Leu  
210 65 70 75 80  
211  
212 Phe Cys Asp Phe Gly Ser Pro Ala Asn Arg Lys Ile Gly Val Cys Thr

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213 85 90 95  
214  
215 Ala Lys Asp Gly Ala Pro Cys Ile Phe Gly Gly Thr Val Tyr Arg Ser  
216 100 105 110  
217  
218 Gly Glu Ser Phe Gln Ser Ser Cys Lys Tyr Gln Cys Thr Cys Leu Asp  
219 115 120 125  
220  
221 Gly Ala Val Gly Cys Met Pro Leu Cys Ser Met Asp Val Arg Leu Pro  
222 130 135 140  
223  
224 Ser Pro Asp Cys Pro Phe Pro Arg Arg Val Lys Leu Pro Gly Lys Cys  
225 145 150 155 160  
226  
227 Cys Glu Glu Trp Val Cys Asp Glu Pro Lys Asp Gln Thr Val Val Gly  
228 165 170 175  
229  
230 Pro Ala Leu Ala Ala Tyr Arg Leu Glu Asp Thr Phe Gly Pro Asp Pro  
231 180 185 190  
232  
233 Thr Met Ile Arg Ala Asn Cys Leu Val Gln Thr Thr Glu Trp Ser Ala  
234 195 200 205  
235  
236 Cys Ser Lys Thr Cys Gly Met Gly Ile Ser Thr Arg Val Thr Asn Asp  
237 210 215 220  
238  
239 Asn Ala Ser Cys Arg Leu Glu Lys Gln Ser Arg Leu Cys Met Val Arg  
240 225 230 235 240  
241  
242 Pro Cys Glu Ala Asp Leu Glu Glu Asn Ile Lys Lys Gly Lys Lys Cys  
243 245 250 255  
244  
245 Ile Arg Thr Pro Lys Ile Ser Lys Pro Ile Lys Phe Glu Leu Ser Gly  
246 260 265 270  
247  
248 Cys Thr Ser Met Lys Thr Tyr Arg Ala Lys Phe Cys Gly Val Cys Thr  
249 275 280 285  
250  
251 Asp Gly Arg Cys Cys Thr Pro His Arg Thr Thr Thr Leu Pro Val Glu  
252 290 295 300  
253  
254 Phe Lys Cys Pro Asp Gly Glu Val Met Lys Lys Asn Met Met Phe Ile  
255 305 310 315 320  
256  
257 Lys Thr Cys Ala Cys His Tyr Asn Cys Pro Gly Asp Asn Asp Ile Phe  
258 325 330 335  
259  
260 Glu Ser Leu Tyr Tyr Arg Lys Met Tyr Gly Asp Met Ala  
261 340 345

PAGE: 1

SEQUENCE VERIFICATION REPORT  
PATENT APPLICATION US/07/752,427

DATE: 09/11/91

TIME: 09:53:06

LINE ERROR

ORIGINAL TEXT

28 Wrong application Serial Number

(A) APPLICATION NUMBER: US



PAGE: 1

SEQUENCE MISSING ITEM REPORT  
PATENT APPLICATION US/07/752,427

DATE: 09/11/91  
TIME: 09:53:06

MANDATORY IDENTIFIER THAT WAS NOT FOUND

PRIOR APPLICATION DATA  
APPLICATION NUMBER  
FILING DATE

PAGE: 1

SEQUENCE CORRECTION REPORT  
PATENT APPLICATION US/07/752,427

DATE: 09/11/91

TIME: 09:53:06

LINE ORIGINAL TEXT

CORRECTED TEXT